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OM nucleic - nucleic search, using sw model

Run on: June 17, 2003, 11:16:03 ; Search time 239.981 Seconds
(without alignments)
10331.847 Million cell updates/sec

Title: US-09-807-933B-4

Perfect score: 1101
Sequence: 1 atgaagcttactactatc.....caggtgtcagaagaataa 1101

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

N Geneseq 101002:*

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24: /SIDS2/gcgdata/geneseq/geneeqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1101	100.0	1101	21	AAA62727
2	1101	100.0	1101	24	AAI43245
3	763	69.3	1017	21	AAA62726
4	763	69.3	1017	24	AAI43244
5	519	47.1	1083	21	AAA62728
6	519	47.1	1083	24	AAI43246
7	421.2	38.3	1043	21	AAA62732
8	421.2	38.3	1043	24	AAI43250
9	390.2	35.4	1164	21	AAA62730

10	390.2	35.4	1164	24	AAI43248
11	367.4	33.4	1017	21	AAA62729
12	367.4	33.4	1017	24	AAI43247
13	289.6	26.3	1041	21	AAA62731
14	289.6	26.3	1041	24	AAI43249
15	194.2	17.6	1473	13	AAQ14857
16	194.2	17.6	1473	13	AAQ26407
17	194.2	17.6	1473	13	AAQ26382
18	194.2	17.6	1473	13	AAQ25933
19	194.2	17.6	1473	13	AAQ29935
20	194.2	17.6	1473	13	AAQ49942
21	194.2	17.6	1473	16	AAV26019
22	194.2	17.6	1473	19	AAV16103
23	192.6	17.5	1473	14	AAQ41733
24	190	17.3	984	19	AAV16105
25	181.2	16.5	1423	17	AAV19049
26	178	16.2	927	17	AAV19062
27	177.8	16.1	960	17	AAV19047
28	177.8	16.1	1132	17	AAV19053
29	177.2	16.1	928	19	AAV15074
30	176.8	16.1	894	17	AAV19061
31	174.4	15.8	922	19	AAV15073
32	166.4	15.1	922	19	AAV15072
33	166	15.1	1154	17	AAV19048
34	163.8	14.9	913	17	AAV19051
35	162	14.7	885	17	AAV19075
36	161.6	14.7	915	19	AAV15075
37	158.8	14.4	1174	17	AAV19050
38	158.8	14.4	1174	19	AAV19096
39	154.6	14.0	1261	19	AAV23748
40	151.6	13.8	925	19	AAV15076
41	150.4	13.7	1058	13	AAQ26405
42	150.4	13.7	1060	12	AAQ14856
43	150.4	13.7	1060	13	AAQ26380
44	150.4	13.7	1060	13	AAQ25932
45	150.4	13.7	1060	13	AAQ29934

ALIGNMENTS

RESULT 1
ID AAA62727 standard; DNA; 1101 BP.
AAA62727
AC AAA62727;
DT 25-SEP-2000 (first entry)
DE Endoglucanase nucleotide sequence 2.
KW Endoglucanase; cellulose breakdown; produce pulp; papermaking;
KW animal foodstuff; ss.
OS Rhizopus oryzae.
PN WO200024879-A1.
PD 04-MAY-2000.
PF 25-OCT-1999; 99WO-JP05884.
PR 23-OCT-1998; 98JP-0302387.
PA (MEIJU) MEIJU SEIKA KAISHA LTD.
PI Nakamura Y, Moriya T, Baba Y, Yanai K, Sumida N, Niehimura T;
PI Murakami K, Nakane A, Yaguchi T, Koga J, Murakami T, Kono T;
DR WPI: 2000-365117/31.
DR P-PSDB; AAB09822.
PT Endoglucanases of fungal origin with high activity under alkaline


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Db 188 CTGSAAGCAGTGGCAATTAATCTCTGAAAGTCTCACAGAAAGTCACTACACTGCTGCTC 247
QY 376 -----ACTACCACTGCTCCCTAGGAATTA 403
Db 248 ACAAGAGAAGTACTACACGCTGCTCATMAAAGACTACACTGCTCTCTAGGAAGACTA 307
QY 404 CAACTACTGCAAGAGTCAAACTCTTCTACTCT-----AGCGGCAAAATACT 451
Db 308 CAACTCTTCCAAAGTTCACCCCTTCTACTAGCTCTAGCTCCAGCGGCAAAATATT 367
QY 452 CCATTGCTCTGAGTGTGCTCTGCTGTAACGCTGTCACTACTGTTATTGGATTGCTGTA 511
Db 368 CCGCTGCTCTGAGTGTGCTCTGCTGTAACGCTGTCACTACTGTTATTGGATTGCTGTA 427
QY 512 AGGCTCTCTGAGTGTGCTCTGCTGTAACGCTGTCACTACTGTTATTGGATTGCTGTA 571
Db 428 AGGCTCTCTGAGTGTGCTCTGCTGTAACGCTGTCACTACTGTTATTGGATTGCTGTA 487
QY 572 AGATGAGTGTCACTGCTCTTACTAGTACAGCAATGTCCAAAGTGGCTGTAAACGCTGTAA 631
Db 488 AGATGAGTGTCACTGCTCTTACTAGTACAGCAATGTCCAAAGTGGCTGTAAACGCTGTAA 547
QY 632 GTTACATGTGTAAAGCAACAGCTGTGGCTGTAAACGATTAATCTTGGCTTATGTTTGG 691
Db 548 GTTACATGTGTAAAGCAACAGCTGTGGCTGTAAACGATTAATCTTGGCTTATGTTTGG 607
QY 692 CTGCTGCTGCACTGAGTGTGCTGTGTAATCTGCTGCTGTGCTGTTGTTGCAACTTA 751
Db 608 CTGCTGCTGCACTGAGTGTGCTGTGTAATCTGCTGCTGTGCTGTTGTTGCAACTTA 667
QY 752 CTTTCACCTTCTACTCTGTTGTCTGTAGAGAGATGTATCCAAAGTCACTAACTGCTG 811
Db 668 CTTTCACCTTCTACTCTGTTGTCTGTAGAGAGATGTATCCAAAGTCACTAACTGCTG 727
QY 812 GTGATCTTGGCTCTCTACTAGTGTCTCACTTTGACCTGCAAAAGCCCGGTGGTGGTGG 871
Db 728 GTGATCTTGGCTCTCTACTAGTGTCTCACTTTGACCTGCAAAAGCCCGGTGGTGGTGG 787
QY 872 GTATTTTCATGAGTGTGCTCCAAAGCAATGGGCTCTCCCAATGACGCTTGGGCTCAAGAT 931
Db 788 GTATTTTCATGAGTGTGCTCCAAAGCAATGGGCTCTCCCAATGACGCTTGGGCTCAAGAT 847
QY 932 ACCGCTGATTTTCTTCTGCACTGTGCTGTCTGTTCTTCCGCACTCCAGCTGCTT 991
Db 848 ACCGCTGATTTTCTTCTGCACTGTGCTGTCTGTTCTTCCGCACTCCAGCTGCTT 907
QY 992 GTAAATGAGATTCATGCTGTCAAGAACGCTGTATACCCAGATGACTTACAGAGAG 1051
Db 908 GTAAATGAGATTCATGCTGTCAAGAACGCTGTATACCCAGATGACTTACAGAGAG 967
QY 1052 TTACCTGTCCCAAGAAATCACCGCCCAAGACAGGTTTTCAGAAATTA 1101
Db 968 TTACCTGTCCCAAGAAATCACCGCCCAAGACAGGTTTTCAGAAATTA 1017

RESULT 4
AAL43244
ID AAL43244 standard; DNA; 1017 BP.
XX
AC AAL43244;
XX
DT 22-AUG-2002 (first entry)
XX
DE Rhizopus arrhizus endoglucanase-related coding sequence 1.
XX
KW Zygomycetes-originated endoglucanase; cellulose binding domain;
XX fibre processing; waste paper de-inking; paper pulp; ds; gene.
XX
OS Rhizopus arrhizus.
XX
XX MO200242474-A1.
XX
XX 30-MAY-2002.

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XX PF 21-NOV-2001; 2001MO-JP10188.
XX PR 21-NOV-2000; 2000JP-0354296.
XX PA (MEIJU) SEIKA KAISHA LTD.
XX PI Nakane A, Baba Y, Koga J, Kubota H;
XX DR WPI; 2002-471729/50.
XX PS P-PSDB; AA015052.
XX PT Cellulose-binding domain-lacking Zygomycetes-originated endoglucanase,
XX PT with effect of endoglucanase activity enhanced in processing fibers,
XX PT deinking waste paper and improving freeness of paper pulp
XX PS Example 10; Page 56-58; 109pp; Japanese.
XX
XX CC The invention comprises the amino acid and coding sequences of
XX CC zygomycetes-originated endoglucanase enzymes lacking the cellulose
XX CC binding domain. The zygomycetes-originated endoglucanase enzymes of the
XX CC invention have enhanced endoglucanase activity. The zygomycetes-
XX CC originated endoglucanase enzymes of the invention are useful for
XX CC processing fibres, de-inking waste paper and improving the freeness of
XX CC paper pulp - which is particularly applicable in detergent compositions.
XX CC The present DNA sequence represents an endoglucanase-related gene
XX CC sequence of the invention.
XX
SQ Sequence 1017 BP; 240 A; 250 C; 235 G; 292 T; 0 other;

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Query Match 69.3%; Score 763; DB 24; Length 1017;
Best Local Similarity 90.3%; Pred. No. 3.7e-221;
Matches 858; Conservative 0; Mismatches 35; Indels 57; Gaps 2;

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QY 209 CTTCGATGTAGCAAGTGTATGTGTCATGTGTGTGTAGCACTGGAATGCGCTTACT 268
Db 68 CTGCGATGTAGCAAGTGTATGTGTCATGTGTGTGTAGCACTGGAATGCGCTTACT 127
QY 269 GTTGGCAATCTGATTCACCTGTAAAGTAAAGCAATTAATCTTCTCAATGCTTGGCC 328
Db 128 GTTGGCAATCTGATTCACCTGTAAAGTAAAGCAATTAATCTTCTCAATGCTTGGCC 187
QY 329 CTGAAAGCAATGGCAATTAATCTGTGAAGCGCTCAATAAAGCACT----- 375
Db 188 CTGGAAGCAATGGCAATTAATCTGTGAAGCGCTCAATAAAGCACT----- 375
QY 376 -----ACTACACTGCTCCGCTAAGAAATTA 403
Db 248 ACAAGAGAAGTACTACGCTGCTCATMAAAGACTACACTGCTCTCTAGGAAGACTA 307
QY 404 CAACTACTGCAAGAGTTCAAACTCTTCTACTCT-----AGCGGCAAAATACT 451
Db 308 CAACTCTTCCAAAGTTCACCCCTTCTACTAGCTCTAGCTCCAGCGGCAAAATATT 367
QY 452 CCATTGCTCTGAGTGTGCTCTGCTGTAACGCTGTCACTACTGTTATTGGATTGCTGTA 511
Db 368 CCGCTGCTCTGAGTGTGCTCTGCTGTAACGCTGTCACTACTGTTATTGGATTGCTGTA 427
QY 512 AGGCTCTCTGAGTGTGCTCTGCTGTAACGCTGTCACTACTGTTATTGGATTGCTGTA 571
Db 428 AGGCTCTCTGAGTGTGCTCTGCTGTAACGCTGTCACTACTGTTATTGGATTGCTGTA 487
QY 572 AGATGAGTGTCACTGCTCTTACTAGTACAGCAATGTCCAAAGTGGCTGTAAACGCTGTAA 631
Db 488 AGATGAGTGTCACTGCTCTTACTAGTACAGCAATGTCCAAAGTGGCTGTAAACGCTGTAA 547
QY 632 GTTACATGTGTAAAGCAACAGCTGTGGCTGTAAACGATTAATCTTGGCTTATGTTTGG 691
Db 548 GTTACATGTGTAAAGCAACAGCTGTGGCTGTAAACGATTAATCTTGGCTTATGTTTGG 607
QY 692 CTGCTGCTGCACTGAGTGTGCTGTGTAATCTGCTGCTGTGCTGTTGTTGCAACTTA 751
Db 608 CTGCTGCTGCACTGAGTGTGCTGTGTAATCTGCTGCTGTGCTGTTGTTGCAACTTA 667

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Qy	752	CTTTCACCTTCACCTCTGTCGTGGTAAAGAATGGTATATCCAAAGCTACTAACACTGGTG	811
Db	668	CTTTCACCTTCACCTCTGTCGTGGTAAAGAATGGTATATCCAAAGCTACTAACACTGGTG	727
Qy	812	GTGATCTTGCTCTCTACCTGCTGCTACCTTGACTTGCAATGCCCCGTGGTGGTGTG	871
Db	728	GTGATCTTGCTCTCTACTAGTGGTGCTCACTTTGACTTGCAATGCCCCGTGGTGGTGTG	787
Qy	872	GTAATTTTCAAATGCTGCTCCCAAGCAATGGGGTGTCTCCCAATGACGTTGGGGCTCGAGAT	931
Db	788	GTATTTTCAAATGCTGCTCCCAAGCAATGGGGTGTCTCCCAATGACGTTGGGGCTCAAGAT	847
Qy	932	ACGGTGTATTTCTTCTGCGATCGACCTGCTCTAGTCTTCTCCGCACTCCAAAGCTGAT	991
Db	848	ACGGTGTATTTCTTCTGCGATCGACCTGCTCTAGTCTTCTCCGCACTCCAAAGCTGAT	907
Qy	992	GTAATGAGATTCACCTGCTTCAAAGAACGCTGATTAACCCAGATGACTTACAAAGAA	105
Db	908	GTAATGAGATTCACCTGCTTCAAAGAACGCTGATTAACCCAGATGACTTACAAAGAA	967
Qy	1052	TTACCTGTCCTCAAGGAATCAACCGCAAGACGTTGTTCAAAAATAA	1101
Db	968	TTACCTGTCCTCAAGGAATCAACCGCAAGACGTTGTTCAAAAATAA	1017

RESULT 5

ID	AAA62728	standard; DNA; 1083 BP.
AC	AAA62728;	
XX	25-SEP-2000	(first entry)
DE	Endoglucanase nucleotide sequence 3.	
XX	Endoglucanase; cellulose breakdown; produce pulp; papermaking;	
KW	animal feedstuff; ss.	
XX	Rhizopus oryzae.	
OS	WO200024879-A1.	
PN	04-MAY-2000.	
PD	25-OCT-1999;	99WO-UP05884.
XX	23-OCT-1998;	98UP-0302387.
XX	(MEIJ) MEIJI SEIKA KAISHA LTD.	
PA	Nakamura Y, Moriya T, Baba Y, Yanai K, Sumida N, Nishimura T;	
PI	Muraehima K, Nakane A, Yaguchi T, Koga J, Murakami T, Kono T;	
XX	MP1; 2000-365117/31.	
DR	P-PSDB; AAB09823.	
XX	Endoglucanases of fungal origin with high activity under alkaline	
PT	conditions for production of paper pulp and animal feedstuffs -	
XX	Claim 44; Page 113-115; 180pp; Japanese.	
PS	This sequence encodes an endoglucanase protein. The invention relates	
CC	to an endoglucanase of fungal origin which can completely break down	
CC	purified cellulose at a concentration of less than 1mg protein/litre,	
CC	and produces more than 50% breakdown of cellulose at pH 8.5. The	
CC	invention includes endoglucanase protein sequences (see	
CC	AA809845-809850), endoglucanase nucleotide sequences (see	
CC	AAA62726-662732) and primers (AAA62733-662802) which are used in the	
CC	identification of the endoglucanase sequences, and in the construction of	
CC	vectors containing the polynucleotides. The endoglucanase enzymes are	
CC	used for the production of pulp for papermaking and for the production of	
CC	animal foodstuffs.	

[illegible]

Db 937 GACTGTCTAACTTCTTCCCTTCAAGCTGTTGTAAGGATTCGGCTGTTCC 996
 Qy 1015 AAGAACGGGATTAACCAAGCATGACTTACAGAGAGTTACTCTCCCAAGAAATCAC 1074
 Db 997 AAAAAAGCTGATTAACCAACATGACTTACAGAGAGTTACTCTCCCAAGCTTACT 1056
 Qy 1075 GCCAAGACAGTGTCTTCAAGAAATTA 1101
 Db 1057 GCCAAGCTGCTGTTCAAGAAATTA 1083

RESULT 6
 AAL43246
 ID AAL43246 standard, DNA; 1083 BP.
 AC AAL43246;
 XX
 DT 22-AUG-2002 (first entry)
 XX
 DE Rhizopus arrhizus endoglucanase-related coding sequence 3.
 XX
 KW Zymomyces-originated endoglucanase; cellulose binding domain;
 KW fibre processing; waste paper de-inking; paper pulp; ds; gene.
 XX
 OS Rhizopus arrhizus.
 XX
 PN MO200242474-A1.
 XX
 PD 30-MAY-2002.
 XX
 XX 21-NOV-2001; 2001WO-JP10188.
 XX
 PF 21-NOV-2000; 2000JP-0354296.
 PR
 XX (MEIJ) MEIJI SEIKA KAISHA LTD.
 XX
 PA Nakane A, Baba Y, Koga J, Kubota H;
 PI
 XX WPI; 2002-471729/50.
 XX
 DR P-PSDB; AAO15054.
 XX
 XX Cellulose-binding domain-lacking Zymomyces-originated endoglucanase,
 PT with effect of endoglucanase activity enhanced in processing fibers,
 PT deinking waste paper and improving freeness of paper pulp
 PS
 XX Disclosure; Page 65-68; 109pp; Japanese.
 CC
 XX The invention comprises the amino acid and coding sequences of
 CC zymomyces-originated endoglucanase enzymes lacking the cellulose
 CC binding domain. The zymomyces-originated endoglucanase enzymes of the
 CC invention have enhanced endoglucanase activity. The zymomyces-
 CC originated endoglucanase enzymes of the invention are useful for
 CC processing fibers, de-inking waste paper and improving the freeness of
 CC paper pulp - which is particularly applicable in detergent compositions.
 CC The present DNA sequence represents an endoglucanase-related gene
 CC sequence of the invention.
 CC
 XX Sequence 1083 BP; 260 A; 297 C; 231 G; 295 T; 0 other;
 SQ

Query Match 47.1%; Score 519; DB 24; Length 1083;
 Best Local Similarity 69.7%; Pred. No. 4.9e-147;
 Matches 772; Conservative 0; Mismatches 305; Indels 30; Gaps 4;

Qy 1 ATGAAGTTTATTACTTACTTCTTCCGCTCTTGGCTCTCGCCCTTGTGTAAGT 60
 Db 1 ATGAAGTTCTTACTTACTTCTTCCGCTCTTGGCTCTCGCCCTTGTGTAAGT 60
 Qy 61 GCTCTGCTGCTAAATGAGCAAGCTGTAAGTCAAGTGTGTAAGCACTGGAATGCG 120
 Db 61 GCCATGCTGCTGAATGAGCAAGCTTACTACCAATGTAAGTGTGTAAGCACTGGAATG 120
 Qy 121 CCTACTTGTGGCAATCTGATCCACTG-----TAAAGTAAGCAAGATTACTACT 174

Db 121 CCTACTGCTGTAATCTGCTACTTCTGTTGATTATCTGACAAATCTTTTACTTCC 180
 Qy 175 CAATGCTTGGCCCCGTAAAGCAAGGCAATTAAGTCTTGTGAATGAGCAAGTTGATGCT 234
 Db 181 CAATGCTTGGCCCCGTAAAGCAAGGCAATTAAGTCTTGTGAATGAGCAAGTTGATGCT 240
 Qy 235 CAATGCTTGGCCCCGTAAAGCAAGGCAATTAAGTCTTGTGAATGAGCAAGTTGATGCT 294
 Db 241 ACTGAGAGTCCCAAGAGCACTACCACTACTTAAGGTTTCAAGAGCAAGCACTACTGAA 300
 Qy 295 GTAGCAAGCAATTAAGTCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGT 354
 Db 301 GCTCTTGAAGAGCAAGCAAGTCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGT 351
 Qy 355 GAAAGGCTCTAATAAGCAAGTCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGT 414
 Db 352 GAAAGGCTCTAATAAGCAAGTCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGT 399
 Qy 415 AAGCTTCAAACTCTTCTTCAAGTCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGT 474
 Db 400 ACTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 459
 Qy 475 GGTAAAGGCTGCTACTTCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGT 534
 Db 460 GGTAAAGGCTGCTACTTCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGT 519
 Qy 535 AAGGCAATGCTACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 594
 Db 520 AAGGCAATGCTACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 576
 Qy 595 GACAGCAATGCTCAAGTGTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 654
 Db 577 GATTAACAACCTCAAAAGGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTT 636
 Qy 655 CTTGGGCTGTAACGATTAATCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT 714
 Db 637 CTTGGGCTGTAACGATTAATCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT 696
 Qy 715 GGTGAATCTGCTGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 774
 Db 697 AGCGAAGTACTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGT 756
 Qy 775 GGTAAAGGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT 834
 Db 757 GGTAAAGGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGT 816
 Qy 835 GCTCACTTGAATGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 894
 Db 817 GCTCACTTGAATGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 876
 Qy 895 CAATGGGCTGCTCAATGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 954
 Db 877 CAATGGGCTGCTCAATGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 936
 Qy 955 GATGCTGTAAGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1014
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 Qy 1015 AAGAACGGGATTAACCAAGCATGACTTACAGAGAGTTACTCTCCCAAGCATATCACT 1074
 Db 997 AAAAAAGCTGATTAACCAACATGACTTACAGAGAGTTACTCTCCCAAGCATATCACT 1056
 Qy 1075 GCCAAGACAGTGTCTTCAAGAAATTA 1101
 Db 1057 GCCAAGCTGCTGTTCAAGAAATTA 1083

RESULT 7
 AAA62732
 ID AAA62732 standard, DNA; 1043 BP.
 XX
 AC AAA62732;
 XX

DT 25-SEP-2000 (first entry)
 XX Endoglucanase nucleotide sequence 7.
 DE Endoglucanase; cellulose breakdown; produce pulp; papermaking;
 XX animal foodstuff; ss.
 XX Rhizopus oryzae.
 XX WO200024879-A1.
 XX 04-MAY-2000.
 XX 25-OCT-1999; 99WO-JP05884.
 XX 23-OCT-1998; 98JP-0302387.
 XX (MEIJ) MEIJI SEIKA KAISHA LTD.
 XX Nakamura Y, Moriya T, Baba Y, Yanai K, Sumida N, Nishimura T;
 XX Murashima K, Nakane A, Yaguchi T, Koga J, Murakami T, Kono T;
 XX WPI; 2000-365117/31.
 DR Endoglucanases of fungal origin with high activity under alkaline
 PT conditions for production of paper pulp and animal feedstuffs -
 XX
 PS Claim 44; Page 132-134; 180pp; Japanese.
 XX
 CC This sequence encodes an endoglucanase protein. The invention relates
 CC to an endoglucanase of fungal origin which can completely break down
 CC purified cellulose at a concentration of less than 1mg protein/litre,
 CC and produces more than 50% breakdown of cellulose at pH 8.5. The
 CC invention includes endoglucanase protein sequences (see
 CC AA09825-809830), endoglucanase nucleotide sequences (see
 CC AA062726-462732) and primers (AA062733-462802) which are used in the
 CC identification of the endoglucanase sequences, and in the construction of
 CC vectors containing the polynucleotides. The endoglucanase enzymes are
 CC used for the production of pulp for papermaking and for the production of
 CC animal foodstuffs.
 CC
 XX Sequence 1043 BP; 212 A; 370 C; 291 G; 170 T; 0 other;
 XX
 SQ
 Query Match 38.3%; Score 421.2; DB 21; Length 1043;
 Best Local Similarity 72.4%; Pred. No. 2.4e-117;
 Matches 565; Conservative 0; Mismatches 203; Indels 12; Gaps 1;
 QY 334 AGCAATGGCAATTAATCTTGTGAAGCGCTCATTAACGACTACTGCTCCGCT 393
 DB 253 ACCGCTGCCAACAAGACGACGACCGCGCTCAACAAGACTACGACCGCTCCGCC 312
 QY 394 AAGGAATTAACAAGTCTGCCAAGCTTCAACTCTTCACTTGAAGCGC----- 444
 DB 313 AAGAAGACACGACCGCTGCCAAGCTTCACTCCGCTCAACTGACGAGCTGCTTTCG 372
 QY 445 ---AAATCTCATTTGTCTGTGCTGTGCTGTGTAACGGTGTGACATCTGTAATGG 501
 DB 373 GGAAGTACAGCGCTGTCAAGCGGTGCGTACGGGCAAGGGGTCACTACCGCTACG 432
 QY 502 GATTCTGTAAAGCGCTCTGTAGTGGCCGGTAAAGCCCAATGTCAGTTCTCTTCAAG 561
 DB 433 GACTCTGTCAAGGCTTTCGTGCTGTGCGCCGCAAGGCTTAAGTCAAGCTGCTGTCAAG 492
 QY 562 TCTCTTAACAAGATGTGTCTCACTGCGCTTACTGACAGCAATGTCCAAAGTGGCTTAAC 621
 DB 493 TCTCTCAACAAGAGAGCGGTCTCAACCGCTTACTGACATCCCAAGCCGAGTCCGGCTGCAAC 552
 QY 622 GGTGTAAACAGTTACTGTGTAAAGCAACGAGCTGTGGCTGTAAAGATTAATCTTGGC 681
 DB 553 GCGGCACTCTTACATGTGTCAACGACACGAGCTGTGCTGTCAACGACACTTGTCT 612
 QY 682 TATGTTTCTGCTGTCTGCTGCATCAAGTGTGTGTGTAATCTGCTGTGCTTCTTGT 741

DB 613 TACGTTTTCGCTGCCGCTGCCATTAGCGCGGTGCGAGAGCCGCTGCTGCTCTGTC 672
 QY 742 TTGAACTTACTTCACTTCACTTCACTTGTGCTGTGTAAGATGTATTCAGTCACT 801
 DB 673 TTCAAGCTCACTTCACTTCACTTCACTTGTGCTGTGTAAGATGTATTCAGTCACT 732
 QY 802 AACACTGTGTGTATTTTCACTTCACTTCACTTGTGCTGTGTAAGATGTATTCAGTCACT 861
 DB 733 AACACTGTGTGTATTTTCACTTCACTTCACTTGTGCTGTGTAAGATGTATTCAGTCACT 792
 QY 862 GGTGTGTGTGTATTTTCACTTCACTTCACTTGTGCTGTGTAAGATGTATTCAGTCACT 921
 DB 793 GGTGTGTGTGTATTTTCACTTCACTTCACTTGTGCTGTGTAAGATGTATTCAGTCACT 852
 QY 922 GGTGTGTGTGTATTTTCACTTCACTTCACTTGTGCTGTGTAAGATGTATTCAGTCACT 981
 DB 853 GGTGTGTGTGTATTTTCACTTCACTTCACTTGTGCTGTGTAAGATGTATTCAGTCACT 912
 QY 982 CAAGCTGTGTGTATTTTCACTTCACTTCACTTGTGCTGTGTAAGATGTATTCAGTCACT 1041
 DB 913 CAAGCTGTGTGTATTTTCACTTCACTTCACTTGTGCTGTGTAAGATGTATTCAGTCACT 972
 QY 1042 TACAAGAGATTACCTGTGCCAAGAAATCACCCGCAAGACAGCTTTTCAAGAAATTA 1101
 DB 973 TACAAGAGATTACCTGTGCCAAGAAATCACCCGCAAGACAGCTTTTCAAGAAATTA 1032
 RESULT 8
 AAL43250
 ID AAL43250 standard; DNA; 1043 BP.
 AC AAL43250;
 XX
 DT 22-AUG-2002 (first entry)
 XX
 DE Rhizopus arrhizus endoglucanase-related codon-optimised DNA sequence.
 XX
 KM Zygomycetes-originated endoglucanase; cellulose binding domain;
 XX fibre processing; waste paper de-inking; paper pulp; ds; gene.
 XX
 OS Rhizopus arrhizus.
 OS Synthetic.
 PN WO200242474-A1.
 XX
 PD 30-MAY-2002.
 XX
 PF 21-NOV-2001; 2001WO-JP10188.
 XX
 PR 21-NOV-2000; 2000JP-0354296.
 XX
 PA (MEIJ) MEIJI SEIKA KAISHA LTD.
 XX
 PI Nakane A, Baba Y, Koga J, Kubota H;
 XX
 DR WPI; 2002-471729/50.
 XX
 P-PSDB; AAO15052.
 XX
 PT Cellulose-binding domain-lacking Zygomycetes-originated endoglucanase,
 PT with effect of endoglucanase activity enhanced in processing fibers,
 PT deinking waste paper and improving freeness of paper pulp -
 XX
 PS Example 10; Page 84-86; 109pp; Japanese.
 XX
 CC The invention comprises the amino acid and coding sequences of
 CC Zygomycetes-originated endoglucanase enzymes lacking the cellulose
 CC binding domain. The Zygomycetes-originated endoglucanase enzymes of the
 CC invention have enhanced endoglucanase activity. The Zygomycetes-
 CC originated endoglucanase enzymes of the invention are useful for
 CC processing fibres, de-inking waste paper and improving the freeness of
 CC paper pulp - which is particularly applicable in detergent compositions.
 CC The present DNA sequence represents an endoglucanase-related gene
 CC sequence of the invention.

SX Sequence 1043 BP; 212 A; 370 C; 291 G; 170 T; 0 other;

Query Match 38.3%; Score 421.2; DB 24; Length 1043;
Best Local Similarity 72.4%; Pred. No. 2,4e-117;
Matches 565; Conservative 0; Mismatches 203; Indels 12; Gaps 1;

QY 334 AGCAATGGCAATTAACCTTCTGAAAGGCTCATTAACGATACATACATGCTCCGCT 333
DB ACCGCTGCCAC 312
QY 394 AAGAAATTAACAACTACTGCGCAAGCTTCAACCTTCACTCACTGAGGCGC----- 444
DB 313 AAGAAACCAACGACCTGCGCAAGCTTCACTCCCTCACTCACTGAGGCTGCTTGG 372
QY 445 ---AAATACCTATTGTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 501
DB 373 GGAAGTACAGCGCTGTACGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 432
QY 502 GATTGCTGAAGGCTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 561
DB 433 GACTGCTGAAGGCTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 492
QY 562 TCTGTGAACAAAGATGT 631
DB 493 TCTGTGAACAAAGATGT 552
QY 622 GGTGTGAACATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 681
DB 553 GGTGTGAACATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 612
QY 682 TATGT 741
DB 613 TACGCTTGT 672
QY 742 TTGCAACTTACTTACTTACTTACTTACTTACTTACTTACTTACTTACTTACTTACT 801
DB 673 TTGCAACTTACTTACTTACTTACTTACTTACTTACTTACTTACTTACTTACTTACT 732
QY 802 AACACTGT 861
DB 733 AACACTGT 792
QY 862 GGT 921
DB 793 GGT 852
QY 922 GGT 981
DB 853 GGT 912
QY 982 CAAGCTGT 1041
DB 913 CAGGCGGT 972
QY 1042 TACAAGAAAGTATCTGCTCCCAAGAAATACCGCCCAAGACAGAGTGTGTCAAGAAAT 1101
DB 973 TACAAGAAAGTATCTGCTCCCAAGAAATACCGCCCAAGACAGAGTGTGTCAAGAAAT 1032

RESULT 9

AAA62730
ID AAA62730 standard; DNA; 1164 BP.

AC AAA62730;

DT 25-SEP-2000 (first entry)

XX Endoglucanase nucleotide sequence 5.

DE Endoglucanase; cellulose breakdown; produce pulp; papermaking;
KM animal foodstuff; ss.
XX

OS Mucor circinelloides.

PN W0200024879-A1.

PD 04-MAY-2000.

PF 25-OCT-1999; 99WO-JP05884.

PR 23-OCT-1998; 98UP-0302387.

PA (MEIJU) MEIJU SEIKA KAISHA LTD.

PI Nakamura Y, Moriya T, Baba Y, Yanai K, Sumida N, Nishimura T;

PI Murashima K, Nakane A, Yaguchi T, Koga J, Murakami T, Kono T;

DR WPI; 2000-365117/31.

DR P-PSDB; AAB09825.

PT Endoglucanases of fungal origin with high activity under alkaline

PT conditions for production of paper pulp and animal feedstuffs -

PS Claim 44; Page 122-124; 180bp; Japanese.

CC This sequence encodes an endoglucanase protein. The invention relates
CC to an endoglucanase of fungal origin which can completely break down
CC purified cellulose at a concentration of less than 1mg protein/litre,
CC and produces more than 50% breakdown of cellulose at pH 8.5. The
CC invention includes endoglucanase protein sequences (see
CC AA09825-B09830), endoglucanase nucleotide sequences (see
CC AA062726-A62732) and primers (AA062733-A62802) which are used in the
CC identification of the endoglucanase sequences, and in the construction of
CC vectors containing the polynucleotides. The endoglucanase enzymes are
CC used for the production of pulp for papermaking and for the production of
CC animal feedstuffs.

SQ Sequence 1164 BP; 272 A; 289 C; 266 G; 337 T; 0 other;

Query Match 35.4%; Score 390.2; DB 21; Length 1164;

Best Local Similarity 64.2%; Pred. No. 6.6e-108;

Matches 715; Conservative 0; Mismatches 308; Indels 90; Gaps 5;

QY 67 GGTGTGAATGTGAAGTGTGAAGTGTGAAGTGTGAAGTGTGAAGTGTGAAGTGTGAAGT 126
DB 64 GGT 123
QY 127 TGTGTGAATGTGAAGTGTGAAGTGTGAAGTGTGAAGTGTGAAGTGTGAAGTGTGAAGT 180
DB 124 TGTGTGAATGTGAAGTGTGAAGTGTGAAGTGTGAAGTGTGAAGTGTGAAGTGTGAAGT 183
QY 181 CTGCGCCGTAAGCAACGCGCATTAAGTCTTGTGAATGTGAAGTGTGAAGTGTGAAGT 240
DB 184 ATTCCCAACCCAGGTTCTCTCTCATCATCATCATCATCATCATCATCATCATCATCAT 243
QY 241 GGTGTGAAGTGTGAAGTGTGAAGTGTGAAGTGTGAAGTGTGAAGTGTGAAGTGTGAAGT 294
DB 244 GGTGTGAAGTGTGAAGTGTGAAGTGTGAAGTGTGAAGTGTGAAGTGTGAAGTGTGAAGT 303
QY 295 GTTGAAGTGTGAAGTGTGAAGTGTGAAGTGTGAAGTGTGAAGTGTGAAGTGTGAAGT 354
DB 304 GAAAGCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 363
QY 355 GAAAGGCTCATTAAGCACTACTACG----- 381
DB 364 GCTTGAAGTGTGAAGTGTGAAGTGTGAAGTGTGAAGTGTGAAGTGTGAAGTGTGAAGT 423
QY 382 -----ACTGCTCCGCTTAAGAAATTAACAT 408
DB 424 ACTGTCAACCAAGCAAGTGAACCAAGCAAGTGAACCAAGCAAGTGAACCAAGCAAGTGAAC 483
QY 409 ACTGTCAACCAAGTGAACCAAGTGAACCAAGTGAACCAAGTGAACCAAGTGAACCAAGT 468
DB 484 ACTGTCAACCAAGTGAACCAAGTGAACCAAGTGAACCAAGTGAACCAAGTGAACCAAGT 543

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Qy 469 GCCTCTGTAAAGGTGTCAGTCTGTTATTGGATTGCTGTAAGGCTCTGTAGCTGG 528
   |||||
Db 544 AATCTGGCAGTGGTTCCACAACCTGTTATTGGATTGTTAAAGCTTCTTGACGCTGG 603
   |||||
Qy 529 CCCGGTAGGCGCAATGTCAATGTTCTCTGCAAGTCTCTTAACAAAGATGTTGCTACC 588
   |||||
Db 604 CTTGAAAAGCTTCTGTCAGTCTGTTGCAACCTGTGCTCCAAATGATATCTCT--- 660
   |||||
Qy 589 CTTAGTGAAGCAGATGTCCTCAAGTGGCTGTAAAGGCTGTAAACAGTTACATGTAAGAC 648
   |||||
Db 661 TTATTAGATGCCAATGCTCAAGATGGTTGTAACGGTGTAAATGTTATATGTAACAC 720
   |||||
Qy 649 AACCAAGCTTGGGCTGTAAAGATATCTTGCCTATGTTTCTGCTGCTGCTCCATCAGT 708
   |||||
Db 721 AACCAAGCTTGGGCTGTAAAGATATGATGCTGCTTACGTTTCTGCTGCTGCTATGCT 780
   |||||
Qy 709 GGTGCTGTGAATCTCGCTGCTGCTGTTCTTGTTCGAATCTTCACTTCACTTCACTCT 768
   |||||
Db 781 GGTCTCAAGCAAGCTGATGGTGTGTTGCTGTTATGAAATGACCTTCACTTCTGCGCT 840
   |||||
Qy 769 GTTGCTGTGAAGATGGTGTATCCAGTCACTAACCTGATCTGCTGCTCTCT 828
   |||||
Db 841 GCTTCTGAAAAGATGGTGTGTCAAGTATCAACCAACCGGTGCGAATTTAGGCTC--- 896
   |||||
Qy 829 ACTGCTGCTCACTTGTGATTCGAATGCGCGTGGTGGTGTGTTGATTTTCAATGTTGC 888
   |||||
Db 897 -----TACCACTTGTGATTCGAATGCGCGTGGTGGTGTGTTGATTTTCAATGCTCT 951
   |||||
Qy 889 TCCAAGCAATGGGCTGCTCCCAATGACGTTGGGGCTGAGAACGCTGTTATTTCTTCT 948
   |||||
Db 952 GCTGCTCAATGGGGCTGCTCCCAATGATGCTGGGAGTAGAATAGTGGTGTGCTAGCTCT 1011
   |||||
Qy 949 GCATCTGCTGCTGCTAGTCTTCTCTGCGACCTCCAGCTGGTGTAAATGAGATTCAC 1008
   |||||
Db 1012 GCTCTGCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1071
   |||||
Qy 1009 TGGTTCAAGAACGCTGATATCCCAAGCATGATGATTCGAAGAACTTACCTGCTCCAGGAA 1068
   |||||
Db 1072 TGGTTCAAGAACCTGATATCCCAAGCATGATGATTCGAAGAACTTACCTGCTCTGTA 1131
   |||||
Qy 1069 ATCACCGCCAAAGACAGTGTTCAGAAATTA 1101
   |||||
Db 1132 TTAATCTACTCGCTCAGTTGGCAAGAAATTA 1164
   |||||

RESULT 10
AAL43248
ID AAL43248 standard; DNA; 1164 BP.
XX
AC AAL43248;
XX
DT 22-AUG-2002 (first entry)
XX
DE Rhizopus arrhizus endoglucanase-related coding sequence 5.
XX
KW Zygomycetes-originated endoglucanase; cellulose binding domain;
KM fibre processing; waste paper de-inking; paper pulp; ds; gene.
XX
OS Mucor circinellloides.
XX
PN MO200242474-A1.
PD 30-MAY-2002.
XX
PF 21-NOV-2001; 2001WO-JP10188.
XX
PR 21-NOV-2000; 2000JP-0354296.
XX
PA (MEIJI) MEIJI SEIKA KAISHA LTD.
XX
PI Nakane A, Baba Y, Koga J, Kubota H,
XX
DR WPI; 2002-471729/50.

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DR P-PSDB; AAO15056.
XX
PT Cellulose-binding domain-lacking Zygomycetes-originated endoglucanase,
PT with effect of endoglucanase activity enhanced in processing fibers,
PT deinking waste paper and improving freeness of paper pulp -
XX
PS Disclosure; Page 75-78; 109pp; Japanese.
XX
CC The invention comprises the amino acid and coding sequences of
CC zygomycetes-originated endoglucanase enzymes lacking the cellulose
CC binding domain. The zygomycetes-originated endoglucanase enzymes of the
CC invention have enhanced endoglucanase activity. The zygomycetes-
CC originated endoglucanase enzymes of the invention are useful for
CC processing fibres, de-inking waste paper and improving the freeness of
CC paper pulp - which is particularly applicable in detergent compositions.
CC The present DNA sequence represents an endoglucanase-related gene
CC sequence of the invention.
XX
SQ Sequence 1164 BP; 272 A; 289 C; 266 G; 337 T; 0 other;

Query Match 35.4%; Score 390.2; DB 24; Length 1164;
Best Local Similarity 64.2%; Pred. No. 6.6e-108;
Matches 715; Conservative 0; Mismatches 308; Indels 90; Gaps 5;

Qy 67 GCTCTAATATGTACCAAGCTGATGTCATATGTTGGTGAAGACTGGAATGGCCCTACT 126
   |||||
Db 64 GCTCTCTTCTGACCTCTGTCTATGTTCAATGTTGGTGCATTTGGCTGACGTGCTTACA 123
   |||||
Qy 127 TGTTCGAATGTGATTCACCTGTAAAGTAAAGCAAGT-----TACTACTTCATGT 180
   |||||
Db 124 TGTGTGATGTGATGATGACCTGTAAAGCTCAAAAGGATTAATAATATTCTTCAATGT 183
   |||||
Qy 181 CTTGGCCCTGAAGCAACCGCAATAGCTTCTGTAATGTAGCAAGTTGTATGTCATGT 240
   |||||
Db 184 ATTCCAAAACCCAAAGGTTCTCTCTCATCATCATCATGATGTTCCGTATATGATATGC 243
   |||||
Qy 241 GGTGTGAAGAGCTGGAATGGCCCTACTTGTTCGAATGTGATCCACTG-----TAA 294
   |||||
Db 244 GGTGGCAATGATGATGAGTGAACCTACCTGTTGTAAAGTGGCTCTACTTGGTGGTCTCA 303
   |||||
Qy 295 GTAAAGCAAGTATCTACTTCAATGTTCTTCCCTGAAAGCAATGSCAATPAAACTTCT 354
   |||||
Db 304 GAAGCAAAAGTATCTACTTCAATGTTCTTCCCTGAAAGCAATGSCAATGCTGTAAAC 363
   |||||
Qy 355 GAAGGCTCATTAAGCACTACTAAC----- 381
   |||||
Db 364 GCTAGCAGACCAAGAAAGACATCTTACCAAGATCTTACACCGCAAGCTACTGCT 423
   |||||
Qy 382 -----ACTGCTCCGCTTAAAGAAATTAACAAT 408
   |||||
Db 424 ACTGTACACCAAGACAGTAAACCAAGACATCTTACCAAGACATCTTACCAAGACATCT 483
   |||||
Qy 409 ACTGCAAAAGCTTCAAACTTCTTAACTTAGCGGCAATATCTCATTTGTTGGTGT 468
   |||||
Db 484 ACTGCGGCTGCTTCACTTCACTTCACTTCTTCTGCTGTTTCAAGTATCTTGGCGGT 543
   |||||
Qy 469 GCCTCTGTAAAGGTGTCAGTCTGTTATTGGATTGCTGTAAGGCTCTGTAGCTGG 528
   |||||
Db 544 AATCTGCAAGTGTTCACAACTGTTATGGAATGTTTAAAGCTTCTTGACGCTGG 603
   |||||
Qy 529 CCCGGTAGGCGCAATGTCAGTCTCTCTGCTCAAGTCTGTAAAGATGTTGTCACCTCC 588
   |||||
Db 604 CTTGAAAAGCTTCTGTCAGTCTGTTTGAACACTGTGCTCCAAATGATATCTCT--- 660
   |||||
Qy 589 CTTAGTGAAGCAGATGTCCTCAAGTGGCTGTAAAGGCTGTAAACAGTTACATGTAAGAC 648
   |||||
Db 661 TTATTAGATGCCAATGCTCAAGATGGTTGTAACGGTGTAAATGTTATATGTAACAC 720
   |||||
Qy 649 AACCAAGCTTGGGCTGTAAAGATATCTTGCCTATGTTTCTGCTGCTGCTCCATCAGT 708
   |||||
Db 721 AACCAAGCTTGGGCTGTAAAGATATGATGCTGCTTACGTTTCTGCTGCTGCTATGCT 780
   |||||
Qy 709 GGTGCTGTGAATCTCGCTGCTGCTGTTCTTGTTCGAATCTTCACTTCACTTCACTCT 768
   |||||

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Matches 471; Conservative 0; Mismatches 249; Indels 12; Gaps 2;

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QY 370 AGGACTACACGACGCTCCCGCTAAGAAATTAACAATCTCCAAAGCTTCAAACT 429
Db 322 ACTACTACACACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 381
QY 430 TCTAATCTAGGCGCAAAATCTCAATCTCTCTCTCTCTCTCTCTCTCTCTCT 489
Db 382 TCTCTCTCAACACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 441
QY 490 ACTCTCTATTTGGATTTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 549
Db 442 ACCCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 501
QY 550 TCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 609
Db 502 AACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 558
QY 610 AGTGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 669
Db 559 AGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 618
QY 670 GATATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 729
Db 619 GACGACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 678
QY 730 TGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 789
Db 679 TGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 738
QY 790 ATCAAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 849
Db 739 GTCCAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 789
QY 850 CAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 909
Db 790 CAGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 849
QY 910 AATGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 969
Db 850 ACCGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 909
QY 970 CTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1029
Db 910 CTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 969
QY 1030 CCAAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1089
Db 970 CCAAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1029
QY 1090 TCAAGAAATTA 1101
Db 1030 GAGCGCAAGTAA 1041

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RESULT 14

AAL43249 standard; DNA; 1041 BP.

AAL43249;

22-ADG-2002 (first entry)

Phycomyces nitens endoglucanase-related coding sequence.

Zygomycetes-originated endoglucanase; cellulose binding domain;

XX fibre processing; waste paper de-inking; paper pulp; ds; gene.

XX Phycomyces nitens.

XX WO200242474-A1.

XX 30-MAY-2002.

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XX 21-NOV-2001; 2001WO-UP10188.
PF 21-NOV-2001; 2000JP-0354296.
XX 21-NOV-2001; 2000JP-0354296.
PR (MEIJU) MEIJU SEIKA KAISHA LTD.
XX Nakane A, Baba Y, Koga J, Kubota H;
XX WPI; 2002-471729/50.
DR P-PSDB; AAO15057.
XX Cellulose-binding domain-lacking Zygomycetes-originated endoglucanase,
PT with effect of endoglucanase activity enhanced in processing fibers,
PT deinking waste paper and improving freeness of paper pulp
XX Disclosure; Page 81-83; 109pp; Japanese.
XX The invention comprises the amino acid and coding sequences of
CC zygomycetes-originated endoglucanase enzymes lacking the cellulose
CC binding domain. The zygomycetes-originated endoglucanase enzymes of the
CC invention have enhanced endoglucanase activity. The zygomycetes-
CC originated endoglucanase enzymes of the invention are useful for
CC processing fibres, de-inking waste paper and improving the freeness of
CC paper pulp - which is particularly applicable in detergent compositions.
CC The present DNA sequence represents an endoglucanase-related gene
CC sequence of the invention.
SQ Sequence 1041 BP; 225 A; 352 C; 248 G; 216 T; 0 other;
XX
Query Match 26.3%; Score 289.6; DB 24; Length 1041;
Best Local Similarity 64.3%; Pred. No. 2,3e-77;
Matches 471; Conservative 0; Mismatches 249; Indels 12; Gaps 2;
QY 370 AGGACTACACGACGCTCCCGCTAAGAAATTAACAATCTCCAAAGCTTCAAACT 429
Db 322 ACTACTACACACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 381
QY 430 TCTAATCTAGGCGCAAAATCTCAATCTCTCTCTCTCTCTCTCTCTCTCTCT 489
Db 382 TCTCTCTCAACACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 441
QY 490 ACTCTCTATTTGGATTTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 549
Db 442 ACCCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 501
QY 550 TCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 609
Db 502 AACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 558
QY 610 AGTGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 669
Db 559 AGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 618
QY 670 GATATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 729
Db 619 GACGACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 678
QY 730 TGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 789
Db 679 TGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 738
QY 790 ATCAAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 849
Db 739 GTCCAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 789
QY 850 CAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 909
Db 790 CAGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 849
QY 910 AATGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 969
Db 850 ACCGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 909

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